

treatment with prednisolone ( $p=0.04$ ) was significantly higher than in patients with recurrent lupus enteritis.

The wall thickness of the most thickened bowel in patients with recurrent lupus enteritis (mean (SD); 9.0 (3.7) mm) was greater than in patients with non-recurrent lupus enteritis (6.1 (2.6) mm), although the difference was not significant ( $p=0.08$ ). All the five patients with bowel wall thickness  $\geq 9$  mm experienced recurrence. This finding may be considered a high-risk factor for recurrent lupus enteritis.

Cumulative dose and duration of treatment may be influenced by other complications of SLE, including lupus nephritis. In our study, class II lupus nephritis was newly diagnosed during prednisolone tapering in three patients (2/7 in non-recurrent, 1/9 in recurrent group), prolonging the duration of treatment with prednisolone. Despite this confounding variable, the dose and duration of corticosteroids was related more closely to the recurrence of lupus enteritis than laboratory indices, including autoantibody profiles and SLEDAI score reflecting lupus activity.

Successful treatment with high-dose prednisolone and intravenous pulse cyclophosphamide has been reported in many patients with intestinal vasculitis, and immunosuppressants such as cyclophosphamide may be recommended for patients with severe or steroid-resistant lupus enteritis.<sup>4,5</sup> In conclusion, longer treatment with corticosteroids or treatment with additional immunosuppressants may be considered in patients with lupus enteritis and with initial bowel wall thickening  $>9$  mm.

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## Lack of association between signaling lymphocytic activation molecule family member 1 gene and rheumatoid arthritis in the French and Tunisian populations

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**S**ignaling lymphocytic activation molecule family member 1 (*SLAMF1*) is a member of the CD2 immunoglobulin superfamily, which is expressed in T cells, B cells, macrophages and dendritic cells.<sup>1</sup> *SLAMF1* is associated with B cell proliferation and immunoglobulin synthesis.<sup>2</sup> The expression of *SLAMF1* in peripheral blood B cells from patients with rheumatoid arthritis was raised compared with healthy controls,<sup>3</sup> and high expression of this molecule was observed in synovial fluid and tissue of patients with rheumatoid arthritis. Moreover, mice deficient in the *SH2D1A* molecule, which binds to the *SLAMF1* receptor, were susceptible to experimental autoimmune diseases.<sup>4,5</sup> Considering these biological data and the potential role of the *SLAMF1* gene in regulating the immune system, we investigated the candidate gene *SLAMF1* polymorphism, located on chromosome 1 (1q21.3–32.3), in patients with rheumatoid arthritis.

Three *SLAMF1* single-nucleotide polymorphisms were studied: C>A (rs 2295612) located in exon 1, G>C (rs 1809963) located in intron 4 and A>C (rs 3796504) located in exon 7. Firstly, 100 French patients with rheumatoid arthritis (87 women and 13 men; mean age: 32 years) in both parents were studied. Secondly, 103 Tunisian patients (85 women and 18 men; mean age: 50.7 years) and 111 healthy controls (64 women and 47 men; mean age: 54.8 years) were analysed in a case–control study. All patients selected fulfilled the 1987

American College of Rheumatology criteria for rheumatoid arthritis.<sup>6</sup>

The polymerase chain reaction-restriction fragment length polymorphism technique was used for genotyping all samples (*DdeI* for rs2295612; *BslI* for rs1809963; *Hpy188II* for rs3796504; primer sequences and amplification programmes given on request).

Statistical analysis was examined by three different methods: transmission disequilibrium test, genotype relative risk and affected family-based controls. Results from Tunisian control subjects and patients with rheumatoid arthritis were compared using the  $\chi^2$  test and Fisher's exact test. *SLAMF1* haplotypes in the French Caucasian trio and Tunisian population were inferred using Genhunter and Phase 2.1 softwares, respectively.

Allele frequencies for the three single-nucleotide polymorphisms were in accordance with Hardy–Weinberg equilibrium in both Tunisian controls and French family-based controls. Statistical analysis did not show any linkage disequilibrium between these markers in the Tunisian as well as in the French population ( $p>0.05$ ). Transmission disequilibrium test analysis showed that rs2295612, rs1809963 and rs3796504 are not preferentially transmitted from heterozygotic parents to affected offsprings in the French trios with rheumatoid arthritis. Similar results were

**Table 1** Analysis of the signalling lymphocytic activation molecule family member 1 single-nucleotide polymorphisms by affected family-based control, transmission disequilibrium and genotype relative risk tests in 100 French families with rheumatoid arthritis

SNP alleles	Allele frequencies		p Value	TDT		p Value	p Value
	Frequency transmitted	Frequency untransmitted		Transmitted	Untransmitted		
rs 2295612_C	0.79	0.83	0.30	28	36	0.31	0.31
rs 2295612_A	0.21	0.17		36	28	0.31	
rs 1809963_C	0.99	0.995	0.31	1	3	0.31	0.62
rs 1809963_G	0.01	0.005		3	1	0.31	
rs 3796504_C	0.89	0.9	0.74	17	19	0.73	0.08
rs 3796504_A	0.11	0.1		19	17	0.73	

GRR, genotype relative risk; SNP, single-nucleotide polymorphism; TDT, transmission disequilibrium test.

obtained using genotype relative risk and affected family-based control tests (table 1).

Moreover, our results showed the same distribution of *SLAMF1* alleles and genotypes between Tunisian patients and controls ( $p>0.05$ ).

Three different haplotypes (CCC, CCA, ACC) were identified at the *SLAMF1* gene, with a frequency  $>5\%$  in the French and Tunisian populations. Neither a significant disequilibrium of transmission to patients with rheumatoid arthritis nor a significant difference in distribution of these haplotypes between Tunisian patients with rheumatoid arthritis and controls was found.

Our study is the first report to examine the potential role of the *SLAMF1* gene in the susceptibility to rheumatoid arthritis in both the French and Tunisian populations, which indicates that *SLAMF1* polymorphisms do not contribute to susceptibility to rheumatoid arthritis in the studied populations. Our study should be replicated in other populations to confirm our preliminary results. Genotypes are available at <http://www.GenHotel.com>.

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# Palindromic rheumatism: different genetic background implies a distinct disease entity

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Palindromic rheumatism is characterised by multiple, episodic and recurrent attacks of arthritis, accompanied by periarticular inflammation without residual joint damage, occurring at irregular intervals and lasting from a few hours to several days.<sup>1–3</sup>

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The definite pathogenesis and disease entity of palindromic rheumatism has not been clarified until now. We investigated the association of rheumatoid arthritis and palindromic

**Abbreviation:** HLA, human leucocyte antigen